## STIC-Biotech/ChemLib

From: Sent: To: Subject:

Gibbs, Terra Wednesday, March 05, 2003 2:05 PM STIC-Biotech/ChemLib

Sequence search request...

Could you please do a regular search of SEQ ID NO:1 of USSN 09/909775?

Please no EST's and no interference search.

Terra Gibbs #79523 AU 1635 Mailbox 11E12 306-3224

THANK YOU!

Edward Hart Technical Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

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## BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or commer (compliments or complaints) about the scope or the results of the search, please contact the RioTech-C searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4. CM-1 Room 1E01

levant prior art found, search results used as follows:  [ 102 rejection
102 rejection
103 rejection
Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
Foreign Patent(s)
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
elevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Search results were not useful in determining patentability or understanding the inven-
omments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or mary.hale@uspto.g v

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HLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQ
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RDQLSRRSIQMEERLQBQRRTVQDKKKTAGRTSRSNPPKFKGKPPAFKPASFKKNIKT
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Abu-Jawdeh, G.M., Comella, N., Brown, L.F., Tognazzi, K. and Direct Submission
Submitted (252P-1997) Pathology, BIDMC, East Campus, 33
Brookline Avenue, Boston, MA 02215, USA
3. (bases 1 to 2840)
Abu-Jawdeh, G.M., Comella, N., Brown, L.F., Tognazzi, K. and Direct Submission
Submitted (02-MAR-1998) Pathology, BIDMC, East Campus, 33
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-MAR-1998) Pathology, BIDMC, East Campus, 3: Brookline Avenue, Boston, MA 02215, USA Sequence update by submitter On Mar 2, 1998 this sequence version replaced gi:2576419.
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Abu-Jawdeh,G.M., Comella,N., Brown,L.F., Tognazzi,K. Unpublished
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/db_xref="taxon:9606"
/db_trissue_type="endometrium"
258. 1298
/note="frizzled related protein"
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100.0%; Pred. No. 0;
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Bandman,O., Lal,P., Hillman,J.L., Yue,H., Reddy,R., Guegler,K.J. and Baughn,M.R.
Composition for the detection of genes encoding receptors and proteins associated with cell proliferation
Patent: US 6183968-A 108 06-FEB-2001;
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                             TCTCCAGGTGTTTGCTTATGCACTTATAAAATGATTTGAACAAATAAAACTAGGAACCTG
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Location/Qualifiers
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I (bases I to 1767)

RAChael,W.L., Ian.E.J. and Sanjay,K.

Machael,W.L., Ian.E.J. and Sanjay,K.

Member of FRSE family, FRAZZLED

AL PATENT. JP 1999000186-A 1 06-JAN-1999;

SWITHKILDE BEECHAM CORP

OS Unidentified

PN 1999000186-A/1

PD 06-JAN-1999

PF 22-MAY-1998 JP 1998141081

PF 22-MAY-1998 JP 1998141081

PF 22-MAY-1998 JP 1998141081

PF 22-MAY-1999 US 60/04/408,Z6-NOV-1997 US 08/978981 PI

MICHAEL WILLIAM LARK,IAN EDWARD JAMES,SANJAY KUMAR PC

C12N15/09,A61K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/00,PC

A51K38/00,

PC A51K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/395,PC

A51K38/00,

PC A51K38/00,A61K38/00,A61K38/00,A61K38/00,A61K39/395,PC

C12N15/09,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/02,A61K37/
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Patent: JP 2000083683-A 1 28-MAR-2000;
SMITHKLINE BEECHAM CORP
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Pred. No. 0;
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0; Mismatches
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/organism="unidentified"
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Best Local Similarity 99.3%;
Matches 1754; Conservative (
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                                                                          CAGCCGGGCCCACCAGTCGTAGTAATCCCCCCAAACCAAAGGGAAAGCCTCCTGCTCCCA 1226
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ACAGTAGTGGAATGA-TAAAAGATCTTTATGTGTTTATGGTCTGCAGAAGGATTTT
                                     TTTGTAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAGAAGGTGAGTTAA
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PD 28-MAR-2000
PD 28-MAR-2000
PF 17-AGG-1999 JP 1999230635
PR 22-MAY-1997 US 08/978981 PI
MICHAEL WILLIAM LARK, IAN EDWARD JAMES, SANJAY KUMAR PC
C12N15/09, AG1K31/7088, AG1K38/00, AG1K39/395, PC
AG1K39/395, AG1K48/00,
PC AG1K48/00, AG1P19/12, AG1P17/06, AG1P19/10,
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Lark,M.W. James, I.E. and kumar, S.

Lark,M.W. James, I.E. and kumar, S.

Member of FREE family, FRAZLED

Member of FREE family, FRAZLED

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PR 28-MAR-2000

PF 17-AuG-1999 JP 1999230635

PR 22-MAY-1997 US 60/04/408, 26-NOV-1997 US 08/978981 PI

MICHAEL WILLIAM LARK,IAN EDWARD JAMES,SANJAY KUMAR PC

CI2NIS,09, AGIK31/7088, AGIK38/00, AGIK39/395, PC

AGIK39/395, AGIK45/00,

PC AGIK39/395, AGIK45/00,

AGIK39/395, AGIK45/00, AGIP13/12, AGIP17/06, AGIP19/02, AGIP19/10, PC
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ACTICCGACTICCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCA
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                         /organism='Unidentified'
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            Location/Qualifiers
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Pred. No. 0;
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                               Location/Qualifiers
Single;
      Topology: Linear;
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Strandedness:
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Best Local Similarity 96.4
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Db 1941 TTTG 1944

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linear PRI 28-JUL-2000
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ toases 1 to 174241)
Raul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaul, R.K., Zhou, Y., James, R.A., Raymond, C., Haugen, E.D. and
                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1999) Human Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 174241)
                                                                                                                                                                                                                                                                     Large-scale Mapping and Sequencing of Human Chromosome 7 Unpublished 2 (bases 1 to 174241)
                             AC018634 174241 bp DNA linear PRI :
Human Chromosome 7 clone RP11-243E12, complete sequence.
AC018634
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 174241)
Bubb,K.L., Desmarais,C.L., Ramsey,S.A. and Hubley,R.M.
Direct Submission
                                                                                                 AC018634.3 GI:9558607
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Submitted (28-UUL-2000) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA on Jul 28, 2000 this sequence version replaced gi:8050915.

Center: University of Washington Genome Center Center Code: UWCC Quality coverage: 6.32x in Q20 bases; agarose-fp Quality coverage: 6.50x in Q20 bases; sum-of-contigs Summary Statistics
Sequencing vector: M13, X02513; 100% of reads
Sequencing vector: M13, X02513; 100% of reads
Chemistry: Dye-primer-amersham; 66% of reads
Assembly program: Phrap; version 0.999319
Consensus quality: 1773493 bases at least Q40
Consensus quality: 174139 bases at least Q40
Consensus quality: 174231 bases at least Q20 Web site: http://www.genome.washington.edu/UWGC/ Contact: uwgchtgs@u.washington.edu Insert size: 179271; 8.6% error; agarose-fp Insert size: 174241; sum-of-contigs Center project name: HsaChr7 Center clone name: RP11-243E12 (d)s156)

Overlapping Sequences: 5': RP11-605P22 (UWGC:djs708)

5': RP11-buses 3': Mapping in progress

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality - 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Homo sapiens chromosome 7 clone RP11-556H1, WORKING DRAFT SEQUENCE,
36 unordered pleces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 225912)
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Web site:http://genome.wustl.edu/gsc/index.shtml
Project information
Center project name: H.NH0556H01
Sequencing vector: Mi3: 96%
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is
Consensus quality: 215747 bases at least 020
Insert size: 230000; agarose-fp
Insert size: 222412; sum-of-contigs
Quality coverage: 4.15 in 020 bases; agarose-fp
Quality coverage: 4.18 in 020 bases; sum-of-contigs
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170682: contig of 15267 bp in length
170782: gap of unknown length
188136: contig of 17354 bp in length
188236: gap of unknown length
204280: contig of 16044 bp in length
204380: gap of unknown length
225331: contig of 19051 bp in length
225331: gap of unknown length
224771: gap of unknown length
224771: gap of unknown length
225912: contig of 1140 bp in length
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/note-"assembly_name:Contigl3"

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7019. 10026

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18384 .21099
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2123. 3309
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/chromosome="7"
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141859. .155315
155416. .170682
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170783. .188136
/note="assembly_name:Contig42"
188237. .204280
/note="assembly_name:Contig43"
204381. .2243431
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223532 . 224671
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                                                                    Db 216434 CCACAAGAGAGGTATGTCACTCATACTTCCCAGGACATCCACGAGAATATTG
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E28726 1458 bp DNA 11near PAT 18-JUN-2001 NOVel human gene (ATG-1639) similar to secretory protein Frizb. E28726 E28726.1 GI:13025446

E28726 LOCUS DEFINITION ACCESSION VERSION

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REFERENCE AUTHORS

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Novel human gene (ATG-1639) similar to secretory protein Frizb Patent: JP 2000102395-A 1 11-APR-2000;
SMITHKLINE BEECHAM CORP
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PD 11-APR-2000
PR 20-SEP-1999 JP 1999265450
PR 23-MAY-1997 US 60/047626,14-JUL-1997 US 08/892083 PL
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1. .1458
/organism ". Unidentified'
Location/Qualifiers
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llarity 99.0%; Pred. No. 1.8e-256;
Conservative 0; Mismatches 12;
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/organism="unidentified"
/db_xref="taxon:32644"
414 c 409 g 28;
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                                                                                              GIGTAAAAAAGGIGAAAGCCAACITITGGCAACATATCICAGCAAAAACTACAGGTATGITAT
                                                                                                                            TGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTAC
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TCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGTGGA
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Sciurognathi; Muridae;
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Guo, K., Wolf, V., Dharmarajan, A., Feng, Z., Bielke, W.,
Friis, R.R.
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frizzled related
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Rodentia;
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Mammalia; Eutheria;
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Rattus norvegicus
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HLHHSTQENAILAIEQYEELVDVNCSSVLRFFLCAMYAPICTLEFLHDPIKPCKSVCQ
RARDDCEPLMKMYNHSWPESLACDELDVYDRGVCISPEAIVTDLPEDWM
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VOYRETEKSSEVIPRTOVPLITNSSCOCPHILPXODVLMCYBRRSRMALLENCLVEKW
RDOLSKRSTOWEERLOEQORTTQDKKQIASRTSRSNPPKFKGRSPASKPASPKKNIKA
RSAPKKSNPKKSTS
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                                                      Gene is upregulated in Physiological Apoptosis
                                                                                                                                                               Clinical Research, ), Bern 3004, Switzerland
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                                                                                                          Dharmarajan, A., Guo, K., Bielke, W. and
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Pred. No. 5.8e-169;
                                                                                                                                          Direct Submission
Submitted (07-JUL-1997) Department for Cl
University of Bern, Tiefenaustrasse 120,
Location/Qualifiers

    1910
    organism="Rattus norvegicus"

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2 (bases 1 to 1910)
Wolf, V., Artuso, L., Dharmarajan, A.,
Friis, P. Afrizzled related Gene is upregulat
                                                                                                                                                                                                                                                                                                                            /product="frizzled related
/protein_id="AAB65431.1"
/db_xref="GI:2293564"
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/db_xref="taxon:10116"
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Wolf,V., Artuso,L.,
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                                                                ATGAGGTCACAACGGTGGTGGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTC
                                                                           GAACTCAAGTCCCGCTCATTACAAATTCTTCTTGCCAGTGTCCACACATCCTGCCCCATC
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                           GCAAAAACTACAGCTATGTTATTCATGCCAAAATAAAAGCTGTGCAGAGGGGGTGGCTGCA
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HAHBYDGMALLAIDQYEBLUVDVNCSSVLRFFCAMYAPICTLBFLHDDTRPCKSVCO
RARDDCCEPLMKMYNIBSPIACDDELPVYDRGVCISPEAIYTDLPBDWWNITPDDM
VQERSFØADCKRLSPDRCKCKKVKYFTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVV
VQKREFKSLSEIPRYOVPLITNSSCQCPHILPHQDVLIMCYBRRSRMMLLENCLVEKW
RDQLSKRSIQMEERCISPEQQQTTQDKKQIASRTSRTSRSNPPKSKGRPPAPRFPKKNI
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Chang.J.T. Esumi, N., Moore, K., Li, Y., Zhang, S., Chew, C., Goodman, B., Rattner, A., Moody, S., Stetten, G., Campochiaro, P.A.
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/protein_id="AAD12306.1"
/db_xref="G1:4219090"
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/organism="Mus musculus"
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Submitted (29-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Series: IRAK Plate: 67 Row: b Column: 24
This clone was selected for full length sequencing because it
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Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: Soares Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MN Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                         /product="secreted frizzled-related sequence protein 4"
/product="AAH34653.1"
/protein_id="AAH34653.1"
/db_xref="G1:22028398"
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/db_xref="G1:22028398"
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| RARDDCEPLMKMYNHSWPESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMM
| VQBRSTPADCKRESPRCKCKKVRPTLATYLSKNYSYVIHAXIRAVQRSGCNEVTTVV
| DVKEIFKSLSPIPRTQVPLITNSSCQCPHILPHQDVLIMCTEWRSRMMLLENCLVEKW
| RDOLSRRSIQMEERLOGDGVRIQDKKQIASRTSRTSRSNPPKSKGRPPAPKFASPKKN
| IKARSAPKKSNLKKSAS"
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e following selection criteria: matched mRNA g1: 7710093
Location/Qualifiers
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                                                                                                                                                                                                                                                                          Length 1739
                                                                                                                                                                                                                                                                        Score 918.2; DB 10; Length
Pred. No. 1.5e-165;
0; Mismatches 313; Indels
                                                                               /clone_lib="Soares_mammary_gland_NbMMG"
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                                                          /clone="MGC:41113 IMAGE:1364770"
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                                                                                                                                                                                                                                             389
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                            /organism="Mus musculus"
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/map="C57BL/6J"
                                                                                                                                                                                                                                             433 g
                                                                                                                       /codon_start=1
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Best Local Similarity 77.5%;
Matches 1243; Conservative
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TAAACGTCTGAGCCCTGATCGGTGCAAGTGCAAAAAGGTGAAGCCGACCCTGGCAACATA 786
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AF140346.1 GI:7672422
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                                                                                           CTGCAATGAGGTCACAACGGTGGTGGATGTAAAAGAGATCTTCAAGTCCTCATCACCCAT
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/product-frizzled related protein"
/protein_id-"AAF66480.1"
/db_xref-"GI:7672433"
/translation-"MLLSIUARCLMLRLALGVRGAPCEAVRIPMCRHWPWNITRMPN
HLHHSTQENAILAIGQYEELVDVNCSSVLSFFLCAMYAPICTLEFLHDPIRPCRCSVCO
RARDDCEPLMKMYNHSWPESLACDELPVYDRGVCISPEAIVTDLEPDVKWIDITPDMM
VQERSFDADCKHLSPDRCKCKKVKFTLATYLSKNYSYVIHARIRAVQRSGCNEVTTVV
DVKEIFRSSSPIPRTQVPLITNSSCQCPHILENGDVLIMCYBERSRAMILLENGLVTVW
RDQLSRRSTQWEERLQBCQCRTTQDKKQIASRTSSNPPRFRGRSPASRPASFRKNIKA
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                                                                                                                                                                                                                            Direct Submission
Submitted (03-APR-1999) Biology, The Hong Kong University of
Science and Technology, Clear Water Bay, Kowloon, Hong Kong, China
       Rattus norvegicus.
Rattus norvegicus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Yam.J.W., Chan.K.W., Wong,V.K. and Hsiao,W.L.
Transcriptional activity of the promoter region of rat
frizzled-related protein gene
Blochem. Blophys. Res. Commun. 286 (1), 94-100 (2001)
                                                                                                                                                                                                                                                                                                                                    cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                 /strain="Fisher"
/db_xref="taxon:10116"
/db_l_type="p53val135-overexpressing
/note="R6813-8"
246. .1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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Pred. No. 2.2e-163;
0; Mismatches 167;
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Yam, J.W.P. and Hsiao, W.L.W.
Regulation of rat frizzled related
Unpublished
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Yam,J.W.P. and Hsiao,W.L.W.
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ilarity 85.7%;
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                     ORGANISM
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Human; phosphate homeostasis modulation; frizzled related protein-4; PRP-4; gene; phosphate transportation; serum phosphate concentration; hypophosphatemnia; phosphaturia: 1,25-dihydroxy vitamin D deficiency; osteomalacia; phosphate homeostasis related disease; X-linked hypophosphatemnia; rickets; oncogenic osteomalacia; rhabdomyolysis; cardiomyopathy; tumoral calcinosis; renal failure; bone mineralisation; ss.
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The invention comprises a method for modulating phosphate homeostasis in a subject. The method involves altering the activity of the frizzled related protein 4 (FRP 4), or altering the activity of the frizzled phosphate plays a critical role in many cellular processes essential to normal functionality of the human body. Phosphate homeostasis is primarily regulated by the kidney, largely through variation in renal tubular re-absorption of phosphate. Alterations of the phosphate transporting function of the kidney, largely through variation in renal tubular re-absorption of the kidney and subsequent disturbance of serum phosphate concentration of the invention is useful for modulating phosphate phosphate and in a subject. The method of the invention can be used to alleviate oncogenic osteomalacia-associated symptoms (e.g. hypophosphatemila, phosphate homeostasis in a subject. The method of the invention can also be used to treat phosphate homeostasis-related diseases (e.g. rinked hypophosphatemila, low serum concentrations of 1,25-dihydroxy vitamin D and osteomalacia). The method of the invention can also be used to treat phosphate homeostasis-related diseases (e.g. rabadomyolysis, cardlomyopathy, tumoral calcinosis, renal failure and bone mineralisation). The present concentration is the human can be related protein 4 (FRP-4).
                                                                                                                                                                                                                      Modulating phosphate homeostasis in a subject, for alleviating oncogenic osteomalacia-associated symptoms, comprises altering the activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4
                                                                                                Manavalan P,
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12-JAN-2001; 2001US-261438P
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                                                 (GENZ ) GENZYME CORP
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other; 2839 BP; 807 A; 624 C; 649 G; 759 T; 0

Gaps DB 24; Length 2839; ö 0; Indels Query Match
100.0%; Score 2839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2839; Conservative 0; Mismatches

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to modulate breast cancer
an expression profile gene
the gene
                                                                                                                                                                                                                                                                                                     antibody; oestrogen receptor; anti-oestrogen; immune response;
lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2;
BCN5; BCO2; BCX2; BCX3; BCA2; BCR2; BCJ7; BCY3; human; ds.
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 GTCAAGAAAGCAGAAACCATCTCATTTCTAACAGCTGTGTTATATTCCATAGTATGCATT
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useful for inhibiting and treating breast cancer in individuals wh are non-tresponsaty to anti-restrogen and positive for osserogen receptor. Compositions comprising BCH1 or a nucleic acid encoding BCH1 are useful for eliciting an immune response in an individual. The antibodies are also useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple
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 CAGCTATGTTATTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCAC
                            CCCGCTCATTACAAATTCTTCTTGCCAGTGTCCACATCCTGCCCCATCAAGATGTTCT
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Human; osteoblast; stem cell differentiation; bone tissue deposition;
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  TATACATGTTTCATAACCTGCCTCCTTTGCTTGGCCTTTATTGAGATAAGTTTTCCT
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24-APR-2001; 2001US-285691P.
                                                                                                             (GENE-) GENE LOGIC INC.
(PROC ) PROCTER & GAMBLE CO.
osteoporosis; osteopathic;
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                                  WO200250301-A2
                 Homo sapiens
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                 1982 TCTGGATTCCTGTTTTTGGTTACCTGATTTCCATGATCATGATGTTCTTGTCAACACC
                                                                                                            CCAGGACATCCACCCTGAGAATAATTTGACAAGCTTAAAAATGGCCTTCATGTGAGTGCC
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                                         CTCTTAAGCAGCACCAGAAACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAATT
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differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation profiles associated with osteoblast genes and their expression

Claim 1; SEQ ID NO 140; 78pp + Sequence Listing; English

The invention relates to genes and their expression profiles

(a) screening modulators of precursor stem cell differentiation osteoblasts, or bone tissue deposition; (b) diagnosing abnormal deposition of bone tissue, abnormal rate osteoblast formation or osteoporosis; or

a (c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

Monitoring the progression of bone tissue deposition.

Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous daysplasia. The present sequence is that of an osteoblast differentiation associated cDNA marker of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fib.wipo.int/published\_pct\_sequences.

Sequence 2840 BP; 807 A; 625 C; 649 G; 759 T; 0 other;

Gaps DB 24; Length 2840; ö Indels ; 0 Ouery Match 100:0%; Score 2839; Best Local Similarity 100.0%; Pred. No. 0; Matches 2839; Conservative 0; Mismatches

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9 1 AGCGGCCGCTGAATTCTAGGGCGGGTTCGCGCCCCGAAGGCTGAGAGCTGGCCTCCTCG

TGCCCTGTGTGCCAGACGGCGGAGCTCCGCGGCCGGACCCCGCGGGCCCCGGCTTTGCTGCC 61

121 GACTGGAGTTTGGGGGAAGAACTCTCCTGCGCCCCAGAAGATTTCTTCCTCGGGGAAGG 180

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Oy Db	361	GCCCTGGAACATCACGCGGATGCCCAACCACCTGCACCACACACGCGGGGAAGGCCAT 420 	
Oy Dp	421	CCTGGCCATCGACAGTACGAGGACCTGGTGGACGTGGAACTGCAGGCCGTGCTGCTGCTTT 480	
Qy Dp	481	CITCITCIGIGCCATGTACGCCCCATTTGCACCCTGGAGTTCCTGCACGACCCTATCAA 540	
Oy Db	541	GCCGTGCAAGTCGGTGTGCCAACGCGCGCGCGACGCTGCGAGCCCCTCATGAAGATGTA 6	
£	601	CAACCACCAGCCCGAAAGCCTGGCCTGCGACGAGCTGCCTGTCTATGACCGTGGCGT 660	
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6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	721	CACACCAGACATGATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAAACGCCTAAGCCC 780 	
Qy Dp	781	CGATCGGTGCAAGTGTAAAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACTA 840 	
Oy Dp	841	CAGCTATGTTATTCATGCCAAAATAAAGCTGTGCAGAGGGGGGGG	
Oy Dp	901	AACGGTGGTGGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTGGAACTCAAGT 960	
Oy Op	961 962	CCGGCTCATTACAAATTCTTGTGGGGTGTCCACATCCTGCCCCATCAGATGTTCT 1020	
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oy Db	1081	ATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACAGCG 1140	
Oy Dp	1141	GAGAACAGTTCAGGACAAGAAAACAGCCGGGGGCACCAGTCGTAGTAATCCCCCCAA 1200 	
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Oy Db	1261 1262	GAGTGCCCAGAAGAACAAACCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG 1320 	
Oy Db	1321	ACTTCCGACTTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCA 1380	
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1560 1620 1680 1740 1800 1860 1920 1980 2040 2100 2160 2220 2280 2340 2400 2460 2520 1441 2281 2401 2461 1741 1801 2041 2101 2161 1501 1561 1621 1861 1981 2221 AGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTACAATTCGACCT AATATGTGCATTGTAAAATAAATGCCATATTCAAACAAAACACGTAATTTTTTACAGT 1802 TITATGGTCTGCAGAAGGATTTTTGTGAAGGGGATTTTTGAAAAATTAGAGAAGT TCTGGATTCCTGTTTTTTGGTTACCTGATTTCCATGATGATGCTTCTTGTCAACACC CTCTTAAGCAGCACCAGAAACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAATT TGGGATACTTTAATCAGAAAAAAGAACTTATTTGCAGCATTTTATCAACAAATTTCATA ATTGTGGACAATTGGAGGCATTTATTTAAAAAACAATTTTATTGGCCTTTTGCTAACAC AGTAAGCATGTATTTATAAGGCATTCAATAAATGCACAAGGCCCAAAGGAAATAAAATC TTCTTAAGGCTATGCTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGGTTTT GCCCTTTGGTACAGAAGGTGAGTTAAAGCTGGTGGAAAAGGCTTATTGCATTGCATTCAG AGCATATGGAAAATTATAATGTGTTTTTTACCAATGACTTCAGTTTCTGTTTTTAGCTA CTCTTAAGCAGCACCAGAAACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAATT AGTTGGCTAATGCTCAAGTATTTTATACCCACAAGAGAGGTATGTCACTCATCTTACTTC CCAGGACATCCACCCTGAGAATAATTTGACAAGCTTAAAAATGGCCTTCATGTGAGTGCC AAATTTTGTTTTCTTCATTTAAATATTTTCTTTGCCTAAATACATGTGAGAGGAGTTAA ATATAAATGTACAGAGGAAAGTTGAGTTCCACCTCTGAAATGAGAATTACTTGACAGT TTTATGGTCTGCAGAAGGATTTTTGTGATGAAAGGGGGATTTTTTGAAAATTAGAGAAGT 1382 1501 1502 1561 1621 1622 1741 1742 1801 1861 1921 1922 1981 1982 2042 2102 2162 2222 2281 2282 2341 2342 2401 2402 1441 1562 2041 2101 2161 2221 2461 qq g В a ò qq ŏ qq ò g ò Q ò a ò a ò g à a ó 음 ŏ g δ a õ q ò õ qq ò QQ ò ò õ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of expression profiles, nucleic acids and proteins involved in colorectal cancer for diagnosis and prognosis of colorectal cancer and identifying candidate agent and/or targets which modulate colorectal
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                                                                                                                                                                                                                                                                                                                                Colorectal cancer modulator protein; CCMP; human; expression profile; drug screening; diagnosis; prognosis; antibody; vaccine; BCX2; immunogenic; gene therapy; targetting molety; CCMP inhibitor; tumour;
                                                              AGTAAGCATGTATTTATAAGGCATTCAATAAATGCACAACGCCCAAAGGAAATAAAATC
                          ACTCAACAAACTGTTGTGCTATTGGATACTTAGGTGGTTTCTTCACTGACAATACTGAAT
                                                    TCTCCAGGTGTTTGCCTTATGCCTTATAAAATGATTTGAACAAATAAAACTAGGAACCTG
                                                                                       TATACATGTGTTTCATAACCTGCCTCCTTTGCTTGGCCCTTTATTGAGATAAGTTTTCCT
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                  CTATCTAATCCTACTCTCCACTACACAGAGGTAATCACTATTAGTATTTGGCATATTAT
                                                                                                                                                                                                                                                                                                                 Human colorectal cancer modulator protein BCX2 cDNA
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colorectal cancer; for the diagnosis and prognosis of colorectal cancer; and as a target for colorectal cancer therapy. The expression profile nucleic acids used in the methods of the invention encode the CCMPs CZA8, BCX2, CBC1, CBC1, CBC3, CJA8, CAA7, BCN5, COA1, BCN7, COA2, CAA9 and CGA8. The CCMPs (especially CJA8 (AAB23166)) may be used in vaccine compositions, and also to raise antibodies for use as therapeutic agents, or targetting moleties for therapeutic agents in the treatment of colorectal cancer. Inhibitors of CCMP activity may also be used in the treatment of other tumours. CCMP nucleotides, especially those
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                                                                                                                                                                                                                       encoding CJAB, may be used in gene therapy, and in genetic vaccines. Sequences AAA97355-A97371 represent nucleic acid sequences encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCATTTCGCCTGAAGCCATCGTCACGGACCTCCCGGAGGATGTTAAGTGGATAAGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGGCCGCTGAATTCTAGGCCGGGTTCGCGCCCCCGAAGGCTGAGAGCTGCCGCGCTGCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCTTCTGTGCCCATGTACGCGCCCATTTGCACCCTGGAGTTCCTGCACGACCCTATCAA
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                                                                                                                                                                                                                                                                         variety of colorectal cancer modulator proteins.
                                                                                                                                                                                                                                                                                                                                               Score 2837.4;
                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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	Oy 1921 GAAACTTAAAAACAAAATA		DD 1982 TCTGGATTCCTGTTTTTGG	2042 CTCTTAAGCAG	Qy 2101 AGTTGGGTAATGCTCAAGTA	Qy 2161 CCAGGACATCCACCTGAGA		2281		2401	2461	2521		2641	2701	2761	0y 2821 AACATCTCACCGGATTC 	RESULT 5 ABK92118 ID ABK92118 standard; DNA; 2	AC ABK92118; XX XX DT 15-AUG-2002 (first entry	
782 CGATCGGTGCAAGTGTAAAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACTA 841	841 CAGCTATGTTATTCATGCCAAAATAAAAGCTGCCAGGGGGGGG	901 AACGGTG	902 AACGGTGGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGT 961	961 CCGGCTCATTACAAATTCTTGCCAGTGTCCACACATCCTGCCCCATCAAGATGTTCT 1020	1021 CATCATGTGTTACGAGTGGCGTTCAAGGATGATGCTTCTTGAAAATTCCTTAGTTGAAAA 1080   1022 CATCATGTGTTACGAGTGGCGTTCAAGGATGATGTTCTTTGAAAATTGCTTAGTTGAAAA 1081	1081   ATGGAGATCACCTTAGTAAAAATCCATACATGGGAAGAGGCTCCAGGAACAGGG	1141 GAGAACAGTTCAGGACAAGAAGAACAGCGGGGGGGCCACCAGTCGTAGTAATCCCCCCAA 120 11111111111111111111111111111111111	1201 ACCARAGGGAAGCCTCCTGCTCCCAAACCAGCCAGTCCCAAGAACACATTAAAACTAG 1	1261	1321 ACTTCCGACTTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCA 13	1381 TGTGCCCCTTGCCCTAACAACTCACTGCAGTGCTCTTCATAGACACATCTTGCAGCATT1 1440 1382 TGTGCCCCTTGCCCTAACAACACTGCAGTGCTCTTCATAGACACATCTTGCAGCATT1 1441	1441 TICITAAGGCTATGCTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGTTT 1500 	1501 GCCTTTGGTACAGAAGGTGAGTTAAAGCTGGTGGAAAGGCTTATTGCATTGCATTCAG 1560 	1561 AGTAACC          1562 AGTAACC	1621 AATATGTGCATTGTAAAATAAATGCCATATTTGAACAAAACACGTAATTTTTTACAGT 1680 	1681 ATGTTTTATTACCTTTTGATATCTGTTGCAATGTTAGTGATGTTTAAAAATGTGATG 1740 	1741 AAAATATAAAAAGAAGAAGAAGAAGAAGAAGAAGAATGAATGAATAAAAAGATCTTTATGTG 1800 	1801 TTPATGGTCTGCAGAAGGATTTTGTGATGAAGGGGATTTTTGAAAAATTAGAGAAGT 1860 	1861 AGCATATGGAAAATTATAAGGTGTTTTTAGCAATGACTTCAGTTTCTGTTTTTAGCTA 1920 1862 AGCATATGGAAAATTATAATGTGTTTTTTAGCAATGACTTCAGTTTCTGTTTTTAGCTA 1921	
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2100 2101 2160 2280 2281 2340 2341 2400 2401 2460 AAGGCATTCAATAAATGCACAACGCCAAAGGAAATAAAATC 2520 ACTACACAGAGGTAATCACTATTAGTATTTTGGCATATTAT 2580 2640 2820 2161 2461 CCTGCCTCCTTTGCTTGGCCCTTTATTGAGATAAGTTTTCCT 2700 2701 TCTCATTTCTAACAGCTGTGTTATATTCCATAGTATGCATT 2760 2821 AACAGTGAGTTTGTCTGTACCATTAGGAGTTAGGTACTAATT SGTTACCTGATTTCCATGATCATGATGCTTCTTGTCAACACC TTAAATATTTTCTTTGCCTAAATACATGTGAGAGGAGTTAA SAAAGTTGAGTTCCACCTCTGAAATGAGAATTACTTGACAGT SAAAGTTGAGTTCCACCTCTGAAATGAGAATTACTTGACAGT VAAAAAGAACTTATTTGCAGCATTTTATCAACAAATTTCATA CATTTATTTAAAAAACAATTTTATTGGCCTTTTGCTAACAC CATTATTTTAAAAAACAATTTTATTGGCCTTTTGCTAACAC GCACTTATAAAATGATTTGAACAAATAAAACTAGGAACCTG CCTGCCTCTTGCTTGCCCTTTATTGAGTAAGTTTTCCT ATCTCATTTCTAACAGCTGTGTTATATTCCATAGTATGCATT CHATTGGATACTTAGGTGGTTTCTTCACTGACAATACTGAAT CTATTGGATACTTAGGTGGTTTCTTCACTGACAATACTGAAT 2820 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent prostate cancer-associated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosting prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated molvanchering.
                                    mammal; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit
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                                   prostate tumour tissue; human;
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Pred. No. 0;
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            DNA sequence
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100.0%; Pre.
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2001US-286214P.
2001US-0847046.
                                                                                                                                                                                                                                                                                            (EOSB-) EOS BIOTECHNOLOGY INC
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2000US-0733288.
2000US-0733742.
2001US-263957P.
2001US-276791P.
                                                                                                                                       2001WO-US32045
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            cancer-associated
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Matches 2820; Conservative
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P-PSDB; ABG61803.
                                              gene therapy; gene;
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                                   cancer;
                                                                                          WO200230268-A2.
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16-MAR-2001;
16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
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08-DEC-2000;
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1039 1020 1099 1201 GCTCCCAAACCAGCCAGTCCCAAGAACATTAAAACTAGGAGTGCCCAGAAGAGAAAA 1260 840 319 300 379 439 420 499 480 559 619 600 619 999 739 799 859 919 ATCGTCACGGACCTCCCGGAGGATGTTAAGTGGATAGACATCACACCAGACATGATGGTA 720 TCTTGCCAGTGTCCACACATCCTGCCCCATCAAGATGTTCTCATCATGTTACGAGTGG **AAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACAGCGGAGAACAGTTCAGGACAAG** GCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTAGGAGTGCCCAGAAGAACA CGTTCAAGGATGATGCTTCTTGAAAATTGCTTAGFTGAAAAATGGAGAGAGATCAGCTTAGT AAGAAAACAGCGGGGGGCACCAGTCGTAGTAATCCCCCCAAACCAAAGGGAAAGCCTCCT AAACTCTCCTGCGCCCCAGAAGATTTCTTCTCGGCGAAGGGACAGCGAAAGATGAGGGT 141 TICCTCTCCCATCCTAGTGGCGCTGTGCCTGTGGCTGCACCTGGCGCTTGGGCTGCGCGGG AGCCTGGCCTGCGACCAGCTGCTGTCTATGACCGTGGCGTGTGCGTTTGGCCTGAAGCC AAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGTGGATGTAAAA GAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCCCCGCTCATTACAAATTCT TCTTGCCAGTGTCCACACCATCCTGCCCCATCAAGATGTTCTCATCATGTGTTACGAGTGG AAGAAAACAGCCGGCCCCCGTAGTAATCCCCCAAACCAAAGGGAAAGCCTCCT GGCAGGAAGAAGAAGGCGCTTTCTGTCTGCCGGGGTCGCAGCGCGAGAGGGCAGTGCCATG GCGCCCTGCGAGGCGGTGCGCATCCCTATGTGCCGGCACATGCCCTGGAACATCACGCGG GCGCCCTGCGAGCCGGTGCCCATCCCTATGTGCCGGCACATGCCCTGGAACATCACGCGG ATGCCCAACCACCTGCACCACAGCACGCAGGAGGACGCCATCCTGGCCATCGAGCAGTAC CAACGCGCGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAGAGCTGGCCCGAA ATCGTCACGGACCTCCCGGAGGATGTTAAGTGGATAGACATCACACCAGACATGATGGTA CAGGAAAGGCCTCTTGATGTTGACTGTAAACGCCTAAGCCCCGATCGGTGCAAGTGTAAA **AAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACTACAGCTATGTTATTCATGCC** GAGATCTTCAAGTCCTCATCACCATCCCTCGAACTCAAGTCCCGCTCATTACAAATTCT GGCAGGAAGAGAAGGCGCTTTCTGTCTGCCGGGGTCGCAGCGCGAGAGGGCAGTGCCATG TTCCTCTCCATCCTAGTGGCGCTGTGCCTGTGGCTGCACCTGGCGCTGGCGCGTGCGCGGC CAGGAGCTGGTGGACGTGCAGCGCCGTGCTGCGCTTCTTCTTCTTGTGCTAC GCGCCCATITGCACCCTGGAGTTCCTGCACGACCCTATCAAGCCGTGCAAGTCGGTGTGC 1040 1021 1100 1081 1160 721 781 200 260 320 301 380 361 440 421 200 481 260 541 620 601 680 199 740 860 920 980 g

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             AACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAGACTTCCGACTTCCTTACAG
                          GATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCATGTGCCCCTTGCCCTAACA
                                                                               GTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGGTTTGCCCTTTGGTACAGAAGGT
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Composition having probes which comprise part of gene sequence encoding proteins associated with cell proliferation useful as hybridizable array elements in Microarrays to monitor expression of target polynucleotide
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such as adenocarcinoma, leukaemia, lymphoma, melanoma, myelloma, sarcoma and terratocarcinoma etc., immunopathology such as AIDS, Addison's disease, adult respiratory distress syndrome, allergies, anaemia, asthma atherosclerosis and bronchitis etc., neuropathology such as Alzheimer's disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, disease, amnesia, amyotrophic lateral sclerosis, bipolar disorder, sattatonia and cerebral neoplasms etc. The microarray can also be used to investigate an individual's predisposition to a disease such as cancer, immunopathology or neuropathology. Also, the microarray can be used for investigating cellular response to infection, drug treatment etc. The microarray can be used for diagnostics, prognostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics, pharmacogenomics etc. The array can also be used for monitoring disease progression. οĘ used in the diagnosis can pe polynucleotides. The microarray 

Sequence 2009 BP; 549 A; 479 C; 520 G; 461 T; 0 other;

4 252 312 372 432 552 612 627 672 792 133 147 193 207 267 327 387 447 492 507 567 687 807 Gaps 73 87 GGTGTGCCAACGCGCGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAGCTG AGACGGCGGAGCTCCGCGGCCCGGGGCCCCGCCTTTGCTGCCGACTGGAGTTTGG GGGAAGAAACTCTCCTGCGCCCCAGAAGATTTCTTCCTCGGCGAAGGGACAGCGAAAGAT GAGGGTGGCAGGAAGAGA - GCCGCTTTCTGTCTGCCGGGGTCGCAGCGCGAGGGCAG GCGCGCGCGCCCTGCGAGGCGGTGCGCATCCCTATGTGCCGGCACATGCCCTGGAACAT CACGCGGATGCCCAACCACCTGCACACACGCAGGAGAACGCCATCCTGGCCATCGA GCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGCCGTGCTGCGCGTTCTTCTTCTTGTGC CATGTACGCGCCCATTTGCACCCTGGAGTTCCTGCACGACCCTATCAAGCCGTGCAAGTC GCCCGAAAGCCTGCCTGCGACGAGCTGCCTGTCTATGACCGTGGCGTGTCCATTTCGCC Length Indels 28; DB DB Score 1876.2; Pred. No. 0; 0; Mismatches ; Query Match
Best Local Similarity 98.4%;
Matches 1937; Conservative 14 28 74 134 148 194 208 253 268 313 328 373 388 433 148 493 508 553 568 613 628 673 588 748 ð a 셤 g ð g ò 8 ò g ò ó 셤 ò 윱 ò g ò g ò q ò ò δ

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Length 1767;

DB 22;

60.1%;

Similarity

Query Match Local

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FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS; antiarthritic; cerebroprotective; vasotropic; nephrotropic; antiHIV; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine; gene therapy; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                  New FRAZZLED polynucleotides and polypeptides useful for treating or preventing e.g. acute and chronic inflammation, autoimmune disorders, bone and cartilage diseases, cancers, or Alzheimer's disease
                                    1930 AAACAAAATAATAATAAAGAAAAATAAAAAAAGGAGGGGGGCAGACAA
                                                                                                                                                                                                                                          /*tag= a
/product= "FRAZZLED polypeptide"
                                                                                                                                          Human FRAZZLED polypeptide encoding DNA.
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171..1211
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                                                                                       AAC84495 standard; DNA; 1767
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The invention provides a human FRAZZLED polypeptide. The FRAZZLED polynucleotides and polypeptides are useful for treating chronic and acute inflammation (e.g. arthritis, osteoarthritis and other osteopenic conditions), Paget's disease, septicemia, autoimmune diseases, infection, stroke, ischemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), metabolic and other bone diseases, cancer (e.g. bone and cartilage cancers or tumors, lymphoproliferative disorders), atherosclerosis, and probes for cona genomic DNA, to isolate cDNA and genomic clones of chrer genes having high sequence similarity to the FRAZZLED gene, and for chromosome identification. The polypeptides may further be used as immunogens to produce antibodies immunospecific for the FRAZZLED colypeptides, as an immunological or vaccine formulation against the above cited diseases, in screening for agonists and antagonists of the FRAZZLED polypeptides, to configure assays for detecting the effect of adding compounds on the production of FRAZZLED mRNA and protein in cells, and to identify membrane bound or soluble ligand or receptors through cerpensents the DNA encoding the human FRAZZLED polypeptide. Claim 2; Page 11; 37pp; English

Sequence 1767 BP; 468 A; 432 C; 456 G; 411 T; 0 other;

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         ACAGTAGTGGAATGAATGT-TAAAAGATCTTTATGTGTTTATGGTCTGCAGAAGGATTTT
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family. The FRZB family controls signalling and developmental patterning. FRAZIED proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of FRAZIED protein by identifying mutations in the FRAZIED gene, or determining FRAZIED protein by identifying mutations in the FRAZIED gene, or determining FRAZIED protein can be used to screen for agonists and antagonists. PRAZIED proteins can be used to screen for agonists and antagonists which bind the FRAZIED protein by observing the binding, or stimulation or inhibition of FRAZIED cactivity. These can be used in treatment to activate (agonist) or inhibit (antagonist) FRAZIED activity, in addition to direct administration of antisense sequences to prevent expression, or FRAZIED polynucleotides to treat conditions associated with a lack of FRAZIED protein. Gene therapp may also be used to affect endogenous FRAZIED protein gene therapp may also be used to affect endogenous FRAZIED protein gene to immunise and prevent diseases, and for isolating protein production. FRAZIED antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating FRAZIED proteins can be administered directly or as a vaccine to inculate against diseases. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, seteoarthritis, septicemia, autoimmune diseases, infection, stroke, ischemmia, acute respiratory disease of syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.
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as diagnostic reagents and for prevention and treatment of cancer,
Alzheimer's disease and AIDS
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                          "frazzled protein"
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              ACCACCTGCACCACAGCACGCAGGAGAACGCCATCCTGGCCATCGAGCAGTACGAGGAGG
                          TGGTGGACGTGAACTGCAGCGCGGTGCTGCGCTTCTTCTTCTGTGCCATGTACGCGCCCCA
                                 TTTGCACCCTGGAGTTCCTGCACCCTATCAAGCCGTGCAAGTCGGTGTCCAACGCG
                                                            CGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAGGTGGCCCGAAAGCCTGG
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Human; FRAZZLED protein; FRZB; chronic inflammation; acute inflammation; arthritis; osteoarthritis; septicemia; autoimmune disease; cancer; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; renal disorder; restenosis; brain injury; AIDS; cancer; ss.
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                                                         AGCTGGTGGAAAAGGCTTATTGCATTGCATTCAGAGTAACCTGTGTGCATACTCTAGAAG
                                                                                                                 TGTTGCAATGTTAGTGATGTTTTAAAATGTGAT-GAAAATATAATGTTTTTAAG-AAGGA
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/product="partial frazzled protein"
/transl_except= (pos:254..256,aa:Xaa)
/note= "Xaa is unspecified"
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The present sequence encodes partial human FRAZZLED protein from the FRZB family. The FRZB family controls signalling and developmental patterning. FRAZZLED proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of FRAZZLED protein by identifying mutations in the FRAZZLED gene, or determining FRAZZLED protein expression levels. FRAZZLED proteins can be used to screen for agonists and antagonists which bind the FRAZZLED protein or governing the binding, or stimulation or inhibition of FRAZZLED activity. These can be used in treatment to activate (agonist) or inhibit (antagonist) FRAZZLED activity, in addition to direct administration of antisense sequences to prevent expression, or FRAZZLED protein. Gene therapy may also be used to affect endogenous FRAZZLED protein. Gene therapy may also be used to affect endogenous FRAZZLED protein. FRAZZLED antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating FRAZZLED clones or purifying the protein by affinity chromatography. FRAZZLED proteins can be administered directly or as a vaccine to include: choose or purifying and protein as a vaccine to include against diseases. Diseases diagnosed, prevented or treated include: choose or purifying infammation, arthritis, osteoarthritis. 11; FRAZZLED nfection, stroke, ischaemia, acute respiratory disease disorders, restenosis, brain injury, AIDS and cancer. 252 369 429 441 133 141 193 201 261 311 321 381 CGAGCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGCCGTGCTGCGCCTTCTTCTTCTG 489 Gaps 81 TTCTAGGGCGGGTTCGCCCCCCGAAGGCTGAGAGCTGGCGCTGCTGGTGCCCTGTGTGCC 73 septicemia, autoimmune diseases, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory diseas AGACGCCGAGCTCCGCGCCGGACCCCGCGCCCCGTTTGCTGCTGCCGACTTTGG AGACGGGGGGGCGGGCCGGACCCCGGGGCCCCCTTTGCTGCCGACTTTGG GGGAAGAAACTCTCCTGCGCCCCAGAAGATTTCTTCCTCGGCGAAGGGACAGCGAAAGAT 142 GGGAAGAAACTCTCCTGCGCCCCAGAGGATTTCTTCCTCGGCGAAGGGACAGCGAAAGAT GAGGGTGGCAGGAAGAGAA - GGCGCTTTCTGTCTGCCGGGGTCGCAGCGCGCGAGAGGGCAG GAGGGTGGCAGGAAGAAGAAGGCCTTTCTGTCTGCCGGGGTCGCAGCGCGAAAGANGGCAG CATCACGCGGATGCCCAACCACCTGCACCACGCACGCAGGAGAACGCCATCCTGGCCAT TGCCATGTTCCTCTCTCCATCCTAGTGGGGGTGTGCCTGTGGCTG - CACCTGGCGCTGTGGGCG TG-CGCGCGCCCCTGCGAGG-CGGTGCGCATCCCTATGTGCCGGCACATGCCCTGGAA DB 20; Length 1969; 49; Indels Sequence 1969 BP; 504 A; 484 C; 518 G; 458 T; 5 other; Score 1694.8; Pred. No. 0; o; Mismatches 9-10; 25pp; English ö 59.7%; ilarity 96.4%; Conservative 0 Similarity Page syndrome, renal Best Local Sim Matches 1854; Query Match 82 262 370 430 14 194 202 253 312 322 382 g \$X4666666666666666666666668888 ö g ò 염 õ Ď, ò 요. à ò 셤 ò g õ

1089 1320 1380 1500 1560 1041 1221 1264 1461 ATGTTTTATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGATGTTTTAAAATGTGATG 1740 1101 1161 1281 1401 1521 606 921 696 981 681 801 861 CACGCGTCCGAAGAGAACAAAACCGAAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG TACAAATTCTTCTTCTCCAGTGTCCACACATCCTGCCCCATCAAGATGTTCTCATCATGTG 982 TACAAATICTTGTIGCCAGIGTCCACACATCTGCCCCCATCAAGATGTTGTCTGATGTGTG TCAGCTTAGTAAAAGATCCATACAGTGGGAAGAGAGGCTGCAGGAACAGCGGAGAACAGT TCAGGACAAGAAGAAAACAGCCGGGCGCACCAGTCGTAGTAATCCCCCCAAACCAAAGGG AAAGCCTCCTGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTAGGAGT--------GCCCAGAAGAGAACAAACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG ACTTCCGACTTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCA TGTGCCCCTTGCCCTAACAACTCACTGCAGTGCTCTTCATAGACACATCTTGCAGCATTT TTCTTAAGGCTATGCTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGGTAGGTTT AGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTACAATTCGACCT **AATATGTGCATTGTAAATAAATGCCATATTTCAAAACAAAACGTAATTTTTTACAGT** CATGATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAAACGCCTAAGCCCCGATCGGTG CAAGTGTAAAAAGGTGAAGCCAACTTTGGCAACGTATCTCAGCAAAAACTACAGCTATGT TATTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGT GGATGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCAT TTACGAGTGGCGTTCAAGGATGATGCTTCTTGAAAATTGCTTGAAAAAATGGAGAGA GCCCTTTGGTACAGAAGGTGAGTTAAAGCTGGTGGAAAAGGCTTATTGCATTGCATTCAG AGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTACAATTCGACCT 1210 1582 1030 1090 1102 1150 1162 1265 1282 1342 1402 1462 1522 1642 730 742 90 850 862 922 970 1321 1381 1441 1501 1561 622 920 910 1681 q a a οy g ò 염 qq ŏ Pp ŏ Op ολ g ò Dp ò qq ò qq à g δ g g ò g οy ò ð g ò οy ŏ ò

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GTCGGTGTGCCAACGCGCGCGCGACGACTGCGAGCCCCTCATGAAGATGTACAACCACAG GTGGGTGTGCCAACGCGCGCGCGCGACTGCGAGCCCCTCATGAAGATGTACAACCACAG

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610 CTGGCCCGAAAGCCTGCCTGCGACGAGCTGCCTGTCTATGACCGTGGCGTGTGCATTTC 669

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Sequence 1969 BP; 504 A; 484 C; 518 G; 458 T; 5 other;
                                                                                                        represents the partial FRAZZLED nucleotide sequence.
                                                                                                                                                  Score 1694.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                   59.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides and polypeptides are useful for treating chronic and acute inflammation (e.g. arthritis, osteoarthritis and other osteopenic conditions), Paget's disease, septicemia, autoimune diseases, infection, stroke, ischemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), metabolic and other bone diseases, cancer (e.g. bone and cartilage cancers or tumors, lymphoproliferative disorders), atherosclerosis, and Alzhehmer's disease. The polynucleotides may be used as hybridization probes for CDNA and genomic DNA, to isolate cDNA and genomic clones of
                                                                                                                 1913
                                FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS; antiarthritic; cerebroprotective; vasotropic; nephrotropic; antiHIV; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine;
1702 ATG-TITATTACCTTTTGATATCTGTTGTTGCAATGTTAGTGATGTTAAAATGTGATCG 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New FRAZZLED polynucleotides and polypeptides useful for treating or preventing e.g. acute and chronic inflammation, autoimmune disorders, bone and cartilage diseases, cancers, or Alzheimer's disease
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                                                                               TGTTTATGGTCTG-CAGAAGGATTTTTGTGATGAAGGGGGATTTTTTGAAAAA--TTAGA
                        AAAATATAATGTTTTTAAGAAGGAACAGTAGT-GGAATGAATGT-TAAAAGATCTTTATG
                                                                                                                 GAAGTAGC - - ATATGGAAAATTATAATGTGTTTTTTTACCAATGACTTCAGTTTCTGTTT
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/note= "Xaa is unknown"
                                                                                                                                                                                                                                                                                                                 Partial nucleotide sequence of human FRAZZLED gene.
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other genes having high sequence similarity to the FRAZZLED gene, and for chromosome identification. The polypeptides may further be used as munnosome identification. The polypeptides may further be used as polypeptides, as an immunological immunospecific for the FRAZZLED polypeptides, as an immunological or vaccine formulation against the above cited diseases, in screening for agonists and antagonists of the PRAZZLED polypeptides, to configure assays for detecting the effect of adding compounds on the production of FRAZZLED mank and protein in cells, and to identify membrane bound or soluble ligand or receptors through standard ligand/receptor binding techniques. The present sequence
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                862 TATICATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGT
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casteoblasts, or bone tissue deposition;

(b) dagnosing abnormal deposition;

(c) dagnosing abnormal deposition;

(d) dagnosing abnormal deposition of bone tissue, abnormal rate of osteoblast formation or osteoporsis; or

(c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

(c) treating or monitoring treatment of the conditions cited in (b), or monitoring the progression of bone tissue deposition.

(c) treating or monitoring treatment of the conditions of the progression of bone formation or bone loss, conditions of the involve altered bone metabolism (e.g. diopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated CDNA marker of the invention.

(c) specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                   cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      are used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to genes and their expression profiles
                                                                                                                                                                                                                                          osteoblast differentiation related cDNA SEQ ID NO 141.
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Best Local Similarity 96.4%;
Matches 1854; Conservative
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24-APR-2001; 2001US-285691P.
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(PROC ) PROCTER & GAMBLE CO.
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RESULT 11
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1740 1560 1620 1380 1641 1401 1461 1521 1701 TCAGGACAAGAAAAAAAAGCGGGGGGGCGCACCAGTCGTAATCCCCCCAAACCAAAGGG 1221 | TGTTTATGGTCTG-CAGAAGGTTTTTGTGATGAAAGGGGATTTTTTGAAAAA--TTAGA ACTICCGACTICCTIACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGTAAGGCCA ATGTTTTATTACCTTTTGATATCTGTTGCAATGTTAGTGATGTTTAAAATGTGATG AAAATATAATGTTTTTAAGAAGGAACAGTAGT-GGAATGAATGT-TAAAAGATCTTTATG 1821 IGTTTATGGTCTGCCAGAAGGATTTTTGTGATGAAAGGGGATTTTTTGAAAATCTAGGG ----GCCCAGAAGAACAAACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAAAGCGGAG AGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTACAATTCGACCT Human frezzled-like protein; HFLP; frizzled protein family; differentiation-related disorder; agonist; antagonist; antibody; haematopoiesis; wound healing; cancer; inflammatory disorder; autoimmune disease; allergic reaction; ss. AAAGCCTCCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTAGGAGT--Full length clone encoding the human frezzled-like protein.

us-09-909-775-1.rng

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This is the nucleotide sequence of the full length clone encoding the human frezzled-like protein (HFLP), used in the method of the invention. It is a member of the frizzled protein family. It is used in the detection and treatment of differentiation-related disorders. In conditions where HFLP is under-expressed, its agonist is involved in the treatment. Antagonist and antibodies of HFLP are used in the treatment of disorder where HFLP is over-expressed, e.g. the regulation of hemantopoissis, and wound healing. HFLP products are used to develop products for treating e.g. cancers, inflammatory and autoimmune diseases, infectious diseases and allergic
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                               protein"
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                               frezzled-like
                                                                                                                                                                                                                                                                                                                                                     New isolated human frezzled-like protein for treating e.g. cancers, inflammatory and infectious diseases and allergic reactions
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                              "human
                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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97US-0055715.
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233 293 180 353 240 413 300 473 174 Gaps 9 GCTGCCGACTGGAGTTTGGGGGAAGAACTCTCCTGCGCCCCCAGAAGATTTCTTCCTCGG CGAAGGGACAGCGAAAGATGAGGGTGGCAGGAAGAGAA - GGCGCTTTCTGTCTGCCGGGG TCGCAGCGCGAGAGGCCAGTGCTTCCTCCTCCTAGTGCCGCCTGTGCCTGTGGC TGCACCTGGCGCTGGCGTGCGCGGCGCGCCCTGCGAGGCGGTGCGCATCCCTATGTGCC **ACCCCATCCTGCCCATCGAGCAGTACGAGGAGCTGGTGGACGTGAACTGCAGCGCCGTGC** 20; Length 1581; 1; 17; Indels DB Score 1541.2; Pred. No. 0; 2; Mismatches Ouery Match 54.3%; Best Local Similarity 98.7%; Matches 1560; Conservative 115 175 234 294 354 241 414 61 121 181 g a 셤 쉽 g ò ò δ ò ç

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1440 1253 1373 1433 1493 1020 AACAGCGGAGAACAGTTCAGGACAAGAAAACAGCCGGGCGCGCCACCAGTCGTAATC 1193 AAACTAGGAGTGCCCAGAAGAGAACAAACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAA 1200 TAGGTTTGCCCTTTGGTACAGAAGGTGAGTTAAAGCTGGTGGAAAAGGCTTATTGCATTG 1553 CATTCAGAGTAACCTGTGTGCATACTCTAGAAGAGTAGGGAAAATAATGCTTGTTACAAT 1613 CTCAAGTCCCGCTCATTACAAATTCTTCTTGCCAGTGTCCACACATCCTGCCCCATCAAG 1013 ATGTICTCATCATGTGTTACGAGTGGCGTTCAAGGATGATGCTTCTTGAAAATTGCTTAG 1073 TTGAAAAATGGAGAGATCAGCTTAGTAAAAGATCCATACAGTGGGAAGAGAGGCTGCAGG 1133 960 720 780 840 900 420 480 540 600 773 999 833 893 953 AAACTAGGAGTGCCCAGAAGAQAACAAACCCGAAAAGAGTGTGAGCTAACTAGTTTCCAA AGCATTTTTCTTAAGGCTATGCTTCAGTTTTTCTTTGTAAGCCATCACAAGCCATAGTGG AAAACTACAGGTAFGTTAFTCAFGCCAAAATAAAAGCTGTGCAGAGGAGGGGTGCATG AAAACTACAGCTATGTTATTCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATG AGCGGAGACTTCCGACTTCCTTACAGGATGAGGCTGGGCATTGCCTGGGACAGCCTATGT **AAGGCCATGTGCCCTTGCCCTAACAACTCACTGCAGTGCTCTTCATAGACACATGTTGC** CTATCAAGCCGTGCAAGTCGGTGTGCCAACGCGCGCGGGGCGACTGCACTGAAGA AGATGTACAACCACAGCTGGCCCGAAAGCCTGGCCTGCGACGAGCTGCCTGTCTATGACC AGGTCACCACGGTGGTGTTGTAAAAGAGATCTTCAAGTCCTCATCACCCTCATCCTCGAA 1081 1261 1321 1494 1074 1134 1021 1194 1254 1141 1314 1201 1374 1434 1381 361 421 594 481 774 661 834 721 781 954 901 196 1554 534 g δ g ò q qq Op ò q ò g ò qq ò qq ò a ò g ò qu ò qq οy g ò පු õ 셤 ö Ω δŽ ò Q ò ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel nucleic acid sequences (A) that are expressed at high level in prostatic tumor tissue and encode gene products or their fragments. The products of the invention have antitumor activity. Polypeptides (I) encoded by (A) are used: (1) for identifying agents for treatment of prostatic cancer and (ii) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate full-length genes (for gene therapy) and for recombinant production of (I). Which can be used to raise and for recombinant production of (I). Which can be used to raise specific antibodies. (A) are identified by assembly of ESTS (expressed sequence tags) before they are analyzed for expression pattern (tissue specificity). This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTS. AA(33423-23476 represent expressed sequence tags described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid expressed at high level in prostatic tumor tissue and encoded polypeptides, useful for treating cancer and screening for therapeutic agents \,
1441 CATTCAAAGTAACCTGTGTGCATACTCTASAARAGTAGGGAAAATAATGCTTGTTACAAT 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosenthal A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 GTGAACTGCAGCGCCGTGCTGCGC-TTCTTCTTCTGTGCCATGTACGCGCCCATTTGCAC 513
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tissue specificity human; ss.
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                                                                           TTACAGTATGTTTTATTACC 1693
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P-PSDB; AAY48252.
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ATG-1639 imbalance by determining ATG-1639 polypeptide expression levels.

ATG-1639 polypeptides can be used to screen for ATG-1639 agonists and antagonists which can be used in treatment to activate or inhibit

ATG-1639 activity, in addition to direct administration of antisense sequences to prevent expression, or ATG-1639 polypeptides to treat conditions associated with a lack of ATG-1639. Gene therapy may also be used to affect endogenous ATG-1639 expression. ATG-1639 antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating ATG-1639 clones or purifying the polypeptides by affinity chromatography. ATG-1639 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include: heart disease. Diseases cardiovascular diseases; kidney diseases; obesity; insulin resistance; diabetes and Central Nervous System (CNS) diseases. The ATG-1639 clone inheritance to be studied through linkage analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GGGAAGAAACTCTCCTGCGCCCCAGAGGATTTCTTCCTCGGCGAAGGACAGCGAAAGAT 201
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Pred. No. 1.6e-291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ATG-1639 protein; secreted ligand; 7-Transmembrane receptor;
heart disease; hypertension; cardiovascular disease; kidney disease;
obesity; insulin resistance; diabetes; Central Nervous System disorder;
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                                  AAGGGGATTTTTGAAAAAT-TAGAGAAGTAGCATATGGAAAATTATAATGTGTTTTTTT
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P-PSDB; AAW73508.
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23-MAY-1997;
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                                                                                                                                         GCCTCCTGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTAGGAGTGCCCAGAA 1272
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742 GATGGTACAGGAAAGGCCTCTTGATGTTGACTGTAAACGCCTAAGCCCCGATCGGTGCAA 801
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                                                                                                                                                                                                                                                                                                                                                                                            TGTAAAAGAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTAC
                            853 TCATGCCAAAATAAAAGCTGTGCAGAGGAGTGGCTGCAATGAGGTCACAACGGTGGTGG
                 793 GTGTAAAAAGGTGAAGCTATTGGCAACGTATCTCAGCAAAAACTACAGCTATGTTAT
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also concentrate of the invention them (ABQ54131-ABQ56305), and also concentrate of the sequences of the invention. The invention additionally relates to recombinant vectors and host calls comprising human ovarian antigen corporation antigen bolymucleotides against human ovarian antigen and the use of ovarian antigen polymucleotides against human ovarian antigens and the use of ovarian antigen polymucleotides and polympetides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and construction of covarian or breast origin, reproductive system alsorders (e.g., infertinity, disorders of pregnancy, anovulation, oblycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HTV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and variantory disorders (e.g., anaemia), cardiovascular disorders, chood-related disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders, ovarian antigen polypoptides and compounds which modulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present convolunce invention.
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                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 AAANAGAAGCCAACTNGGGCCCCATATCNAAGCAAAANCTACAGCTATGTTATTCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           920 GAGATCTTCAAGTCCTCATCACCCATCCCTCGAACTCAAGTCCCGCTCATTACAAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 1216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
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                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 334; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1140; Conservative
                                                                                                                                                                                                                                                                                 neurological diseases
WPI; 2002-147878/19.
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                                         P-PSDB; ABP41377
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1040 CGTTCAAGGATGATGCTTCTTGAAAATTGCTTAGTTGAAAAATGGAGAGATCAGCTTAGT 1099

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ACAACTCACTGCAGTGCTCTTCATAGACACATGTTGCAGCATTTTTCTTAAGGCTATGCT 1456
                                                                                                                                                                                                                                                                                                              AATAAATGCCATATTTCAAACAAACACGTAATTTTTTACAGTATGTTTTATATACTTT 1696
                                                     1157 AAGAAGAAAACAGCCGGGGGGCCACCAGTCGTAATCCCCCCAAACCAAAGGGAAAGCCT 1216
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                                                                                    CCTGCTCCCAAACCAGCCAGTCCCAAGAAGAACATTAAAACTAGGAGTGCCCAGAAGAGA 1276
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